



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 04:14 AM UTC

PDB ID : 1DGI / pdb_00001dgi
Title : Cryo-EM structure of human poliovirus(serotype 1)complexed with three domain CD155
Authors : He, Y.; Bowman, V.D.; Mueller, S.; Bator, C.M.; Bella, J.; Peng, X.; Baker, T.S.; Wimmer, E.; Kuhn, R.J.; Rossmann, M.G.
Deposited on : 1999-11-24
Resolution : 22.00 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

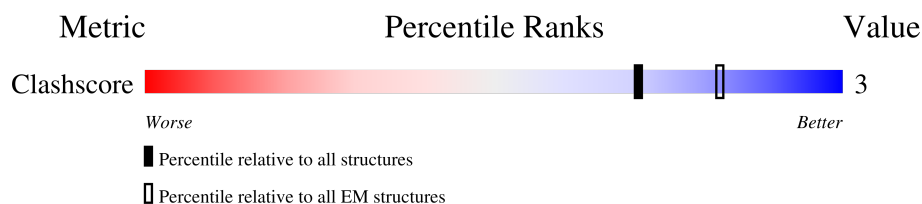
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

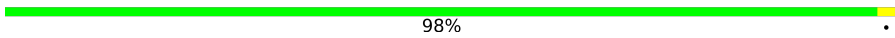
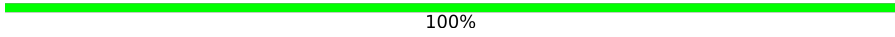
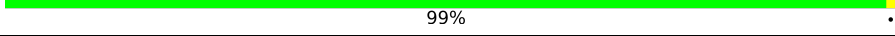
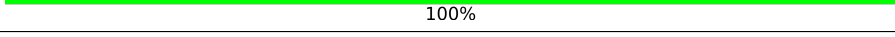
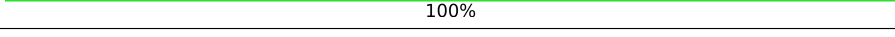
The reported resolution of this entry is 22.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	R	302	 98% .
2	1	288	 100%
3	2	268	 99% .
4	3	235	 100%
5	4	63	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 1155 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called POLIOVIRUS RECEPTOR.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	R	301	Total	C	0	301
			301	301		

- Molecule 2 is a protein called VP1.

Mol	Chain	Residues	Atoms		AltConf	Trace
2	1	288	Total	C	0	288
			288	288		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	6	GLY	LEU	conflict	UNP P03300
1	7	SER	GLU	conflict	UNP P03300
1	9	SER	MET	conflict	UNP P03300
1	10	THR	ILE	conflict	UNP P03300

- Molecule 3 is a protein called VP2.

Mol	Chain	Residues	Atoms		AltConf	Trace
3	2	268	Total	C	0	268
			268	268		

- Molecule 4 is a protein called VP3.

Mol	Chain	Residues	Atoms		AltConf	Trace
4	3	235	Total	C	0	235
			235	235		

- Molecule 5 is a protein called VP4.

Mol	Chain	Residues	Atoms		AltConf	Trace
5	4	63	Total 63	C 63	0	63

3 Residue-property plots [i](#)

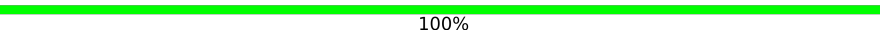
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: POLIOVIRUS RECEPTOR

Chain R:  98%

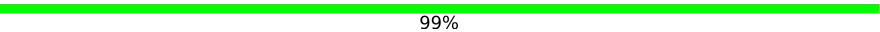


- Molecule 2: VP1

Chain 1:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: VP2

Chain 2:  99%



- Molecule 4: VP3

Chain 3:  100%

There are no outlier residues recorded for this chain.

- Molecule 5: VP4

Chain 4:  100%

There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Xtriage (Phenix) and EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	1.00Å 1.00Å 1.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 22.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-22.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1155	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MYR

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	301	0	0	3	0
2	1	288	0	0	0	0
3	2	268	0	0	1	0
4	3	235	0	0	0	0
5	4	63	0	0	0	0
All	All	1155	0	0	4	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (4) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:69:HIS:CA	1:R:74:SER:CA	2.22	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:150:GLU:CA	1:R:165:ARG:CA	2.54	0.85
3:2:82:LEU:CA	3:2:83:PRO:CA	2.83	0.56
1:R:276:GLY:CA	1:R:312:CYS:CA	2.94	0.46

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.